



IFWO

RAW SEQUENCE LISTING

DATE: 08/30/2004

PATENT APPLICATION: US/10/682,011

TIME: 12:37:43

Input Set : N:\Crif3\RULE60\10682011.raw

Output Set: N:\CRF4\08302004\J682011.raw

1 <110> APPLICANT: Alibhai, Murtaza
 2 Rydel, Timothy
 3 <120> TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
 4 <130> FILE REFERENCE: 38-21 (51842)B
 5 <140> CURRENT APPLICATION NUMBER: US/10/682,011
 6 <141> CURRENT FILING DATE: 2003-10-09
 7 <150> PRIOR APPLICATION NUMBER: US/09/755,274
 8 <151> PRIOR FILING DATE: 2001-01-05
 9 <160> NUMBER OF SEQ ID NOS: 60
 10 <170> SOFTWARE: PatentIn version 3.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 386
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Solanum cardiophyllum
 16 <220> FEATURE:
 W--> 17 <221> NAME/KEY: Protein
 18 <222> LOCATION: (1)..(386)
 19 <223> OTHER INFORMATION: patatin homolog pat17 amino acid sequence
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 22 1 5 10 15
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 24 20 25 30
 25 Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
 26 35 40 45
 27 Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala
 28 50 55 60
 29 Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
 30 65 70 75 80
 31 Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe
 32 85 90 95
 33 Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln
 34 100 105 110
 35 Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys
 36 115 120 125
 37 Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
 38 130 135 140
 39 Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn
 40 145 150 155 160
 41 Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu
 42 165 170 175
 43 Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr
 44 180 185 190

ENTERED

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Input Set : N:\Crf3\RULE60\10682011.raw

Output Set: N:\CRF4\08302004\J682011.raw

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45   Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu
46               195                200                205
47   Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro
48               210                215                220
49   Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro
50               225                230                235                240
51   Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu
52               245                250                255
53   Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala
54               260                265                270
55   Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln
56               275                280                285
57   Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser
58               290                295                300
59   Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln
60               305                310                315                320
61   Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
62               325                330                335
63   Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys
64               340                345                350
65   Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
66               355                360                365
67   Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
68               370                375                380
69   Ser Tyr
70               385

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72 <210> SEQ ID NO: 2

73 <211> LENGTH: 365

74 <212> TYPE: PRT

75 <213> ORGANISM: synthetic

76 <220> FEATURE:

W--> 77 <221> NAME/KEY: Protein

78 <222> LOCATION: (1)..(365)

79 <223> OTHER INFORMATION: Patatin isozyme PatFm (mature protein lacking signal peptide)

80 <400> SEQUENCE: 2

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81   Met Ala Leu Glu Glu Met Val Ala Val Leu Ser Ile Asp Gly Gly Gly
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83   Ile Lys Gly Ile Ile Pro Gly Thr Ile Leu Glu Phe Leu Glu Gly Gln
84               20               25               30
85   Leu Gln Lys Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe
86               35               40               45
87   Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile
88               50               55               60
89   Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Asn Glu Ile
90               65               70               75               80
91   Val Pro Phe Tyr Phe Glu His Gly Pro His Ile Phe Asn Ser Arg Tyr
92               85               90               95
93   Trp Pro Ile Phe Trp Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val
94               100              105              110

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95      Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu
96              115                      120                      125
97      Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe
98              130                      135                      140
99      Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu Asp Ala Lys Thr Tyr
100             145                      150                      155                      160
101      Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro Pro His
102                      165                      170                      175
103      Tyr Phe Ala Thr Asn Thr Ile Asn Gly Asp Lys Tyr Glu Phe Asn Leu
104                      180                      185                      190
105      Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro Ala Leu Leu Ser Val
106                      195                      200                      205
107      Ser Val Ala Thr Arg Arg Ala Gln Glu Asp Pro Ala Phe Ala Ser Ile
108                      210                      215                      220
109      Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly Thr Gly
110                      225                      230                      235                      240
111      Thr Thr Ser Glu Phe Asp Lys Thr His Thr Ala Glu Glu Thr Ala Lys
112                      245                      250                      255
113      Trp Gly Ala Leu Gln Trp Met Leu Val Ile Gln Gln Met Thr Glu Ala
114                      260                      265                      270
115      Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Val Phe Gln Asp
116                      275                      280                      285
117      Leu His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr
118                      290                      295                      300
119      Gly Thr Thr Thr Lys Ala Asp Asp Ala Ser Glu Ala Asn Met Glu Leu
120                      305                      310                      315                      320
121      Leu Ala Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Lys Asp
122                      325                      330                      335
123      Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu
124                      340                      345                      350
125      Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr
126                      355                      360                      365

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128 <210> SEQ ID NO: 3

129 <211> LENGTH: 364

130 <212> TYPE: PRT

131 <213> ORGANISM: synthetic

132 <220> FEATURE:

W--> 133 <221> NAME/KEY: Protein

134 <222> LOCATION: (1)..(364)

135 <223> OTHER INFORMATION: Patatin isozyme PatIm (mature protein lacking signal peptide)

136 <400> SEQUENCE: 3

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137      Pro Trp Leu Glu Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly
138      1              5              10              15
139      Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu Glu Phe Leu Glu Gly Gln
140      20              25              30
141      Leu Gln Glu Val Asp Asn Asn Lys Asp Ala Arg Leu Ala Asp Tyr Phe
142      35              40              45
143      Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile
144      50              55              60

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Input Set : N:\Crf3\RULE60\10682011.raw

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145  Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Asp Ile
146  65                               70                               75                               80
147  Val Pro Phe Tyr Phe Glu His Gly Pro His Ile Phe Asn Tyr Ser Gly
148                               85                               90                               95
149  Ser Ile Leu Gly Pro Met Tyr Asp Gly Lys Tyr Leu Leu Gln Val Leu
150                               100                              105                              110
151  Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val
152                               115                              120                              125
153  Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr
154                               130                              135                              140
155  Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp
156  145                               150                              155                              160
157  Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile Tyr Phe Pro Pro His His
158                               165                              170                              175
159  Phe Val Thr His Thr Ser Asn Gly Ala Arg Tyr Glu Phe Asn Leu Val
160                               180                              185                              190
161  Asp Gly Ala Val Ala Thr Val Gly Asp Pro Ala Leu Leu Ser Leu Ser
162                               195                              200                              205
163  Val Ala Thr Arg Leu Ala Gln Glu Asp Pro Ala Phe Ser Ser Ile Lys
164                               210                              215                              220
165  Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu Ser Leu Gly Thr Gly Thr
166  225                               230                              235                              240
167  Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala Glu Glu Ala Ala Lys Trp
168                               245                              250                              255
169  Gly Pro Leu Arg Trp Met Leu Ala Ile Gln Gln Met Thr Asn Ala Ala
170                               260                              265                              270
171  Ser Phe Tyr Met Thr Asp Tyr Tyr Ile Ser Thr Val Phe Gln Ala Arg
172                               275                              280                              285
173  His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Asn Gly
174                               290                              295                              300
175  Thr Thr Thr Glu Met Asp Ala Ser Glu Ala Asn Met Glu Leu Leu
176  305                               310                              315                              320
177  Val Gln Val Gly Glu Thr Leu Leu Lys Lys Pro Val Ser Arg Asp Ser
178                               325                              330                              335
179  Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser
180                               340                              345                              350
181  Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr
182                               355                              360
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 386
186 <212> TYPE: PRT
187 <213> ORGANISM: synthetic
188 <220> FEATURE:
W--> 189 <221> NAME/KEY: Protein
190 <222> LOCATION: (1)..(386)
191 <223> OTHER INFORMATION: Patatin isozyme PatL+ (including signal peptide)
192 <400> SEQUENCE: 4
193  Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Phe Phe Met Ile Leu Ala
194  1                               5                               10                               15

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Input Set : N:\Crf3\RULE60\10682011.raw

Output Set: N:\CRF4\08302004\J682011.raw

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195      Thr Thr Ser Ser Thr Cys Ala Lys Leu Glu Glu Met Val Thr Val Leu
196                20                25                30
197      Ser Ile Asp Gly Gly Gly Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu
198                35                40                45
199      Glu Phe Leu Glu Gly Gln Leu Gln Glu Val Asp Asn Asn Lys Asp Ala
200                50                55                60
201      Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
202                65                70                75                80
203      Leu Leu Thr Ala Met Ile Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe
204                85                90                95
205      Ala Ala Ala Lys Asp Ile Val Pro Phe Tyr Phe Glu His Gly Pro His
206                100               105               110
207      Ile Phe Asn Tyr Ser Gly Ser Ile Leu Gly Pro Met Tyr Asp Gly Lys
208                115               120               125
209      Tyr Leu Leu Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His
210                130               135               140
211      Gln Ala Leu Thr Glu Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn
212                145               150               155               160
213      Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu
214                165               170               175
215      Asp Ala Lys Met Tyr Asp Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile
216                180               185               190
217      Tyr Phe Pro Pro His His Phe Val Thr His Thr Ser Asn Gly Ala Arg
218                195               200               205
219      Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Gly Asp Pro
220                210               215               220
221      Ala Leu Leu Ser Leu Ser Val Ala Thr Arg Leu Ala Gln Glu Asp Pro
222                225               230               235               240
223      Ala Phe Ser Ser Ile Lys Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu
224                245               250               255
225      Ser Leu Gly Thr Gly Thr Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala
226                260               265               270
227      Glu Glu Ala Ala Lys Trp Gly Pro Leu Arg Trp Met Leu Ala Ile Gln
228                275               280               285
229      Gln Met Thr Asn Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Ile Ser
230                290               295               300
231      Thr Val Phe Gln Ala Arg His Ser Gln Asn Asn Tyr Leu Arg Val Gln
232                305               310               315               320
233      Glu Asn Ala Leu Asn Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu
234                325               330               335
235      Ala Asn Met Glu Leu Leu Val Gln Val Gly Ala Thr Leu Leu Lys Lys
236                340               345               350
237      Pro Val Ser Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg
238                355               360               365
239      Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala
240                370               375               380
241      Ser Tyr
242      385
244 <210> SEQ ID NO: 5

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/682,011

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Input Set : N:\Crf3\RULE60\10682011.raw
Output Set: N:\CRF4\08302004\J682011.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 2,4
Seq#:15; Xaa Pos. 2,3
Seq#:42; Xaa Pos. 3,5

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 79
Seq#:3; Line(s) 135
Seq#:15; Line(s) 820
Seq#:37; Line(s) 1585
Seq#:38; Line(s) 1670
Seq#:40; Line(s) 1760
Seq#:41; Line(s) 1828

VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/682,011

TIME: 12:37:44

Input Set : N:\CrF3\RULE60\10682011.raw

Output Set: N:\CRF4\08302004\J682011.raw

L:17 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:133 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:189 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:249 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:369 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:431 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:493 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:567 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:629 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:691 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:753 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:806 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:818 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:830 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:842 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:854 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
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L:1826 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:1882 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42
L:1886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1894 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1905 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
L:1916 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:1927 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10682011.raw

Output Set: N:\CRF4\08302004\J682011.raw

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L:1960 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:1971 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:1982 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51